1/66

SEQUENCE LISTING

<110>	Juli	Julius-Maximilians-Universitat wurzburg								
<120>	Mill	Millisecond activation switch for seven-transmembrane proteins								
<130>	Н134	0 PCT S3								
<150> <151>		.02 59 874.6 -12 - 19								
<150> <151>		EP 03 00 4394.7 2003-03-03								
<160>	46									
<170>	Pate	entIn versio	n 3.1							
<210> <211> <212> <213>	210> 1 211> 1409 212> DNA									
<400>	1 tacc	catacgacgt	cccagactac	gccagcatgg	gctcactgca	gccggatgcc	60			
		gctggaacgg					120			
		tgacactgac				•	180			
tttggc	aacg	tgctggttat	tatcgcggtg	ttcaccagtc	gcgcgctcaa	agctccccaa	240			
aacctc	ttcc	tggtgtccct	ggcctcagcg	gacatcctgg	tggccacgct	ggtcattccc	300			
ttttct	ttgg	ccaacgaggt	tatgggttac	tggtactttg	gtaaggtgtg	gtgtgagatc	360			
tatttg	gctc	tcgacgtgct	cttttgcacg	tegtecatag	tgcacctgtg	cgccatcagc	420			
cttgac	cgct	actggtccat	cacgcaggcc	atcgägtaca	acctgaagcg	cacgccgcgt	480			
cgcatc	aagg	ccatcattgt	caccgtgtgg	gtcatctcgg	ctgtcatctc	cttcccgcca	540			
ctcatc	tcca	tagagaagaa	gaccagaagt	ggtatgtcat	ctcctcgtcc	atcggttcct	600			
tcttcg	cgcc	ttgcctcatc	atgatcctgg	tctacgtgcg	tatttaccag	atcgccaagc	660			
gtcgca	.cccg	cgtgcctccc	agccgccggg	gtccggacgc	ctgttccgcg	ccgccggggg	720			
gcgccg	atcg	caggcccaac	gggctgggcc	cggagcgcgg	cgcgggtccc	acgggcgctg	. 780			
aggcgg	agcc	gctgcccacc	cagcttaacg	gtgccccggg	ggagcccgcg	cccgccgggc	840			
cccgcg	atgg	ggatgcgctg	gacctagagg	agagttcgtc	gtccgagcac	gccgagcggc	900			
ccccgg	iggcc	ccgcagaccc	gaccgcggcc	cccgagccaa	gggcaagacc	cgggcgagtc	960			
aggtga	agcc	gggggacagt	ctgccgcggc	gegggeeegg	ggccgcgggg	ccgggggctt	1020			
cggggt	ccgg	gcacggagag	gagcgcggcg	ggggcgccaa	agegtegege	tggcgcggga	1080			

2/66

2/00	
ggcaaaaccg ggagaaacgc ttcacgttcg tgctggcggt ggtgatcggc gtgttcgtgg	1140
tgtgttggtt teegttettt tteacetaca egeteatage ggteggetge eeggtgeeca	1200
gccagctctt caacttcttc ttctggttcg gctactgcaa cagctcgctg aaccctgtta	1260
tctacaccat cttcaaccac gacttccgac gcgccttcaa gaagatcctc tgccgtgggg	1320
acagaaaacg catcgtgtga ttcaaccacg acttccgacg cgccttcaag aagatcctct	1380
gccgtgggga cagaaaacgc atcgtgtga	1409
<210> 2 <211> 462 <212> PRT <213> Mouse <400> 2	
Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Met Gly Ser Leu	
1 5 10 15	
Gln Pro Asp Ala Gly Asn Ser Ser Trp Asn Gly Thr Glu Ala Pro Gly 20 25 30	
Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu 35 40 45	
Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val 50 55 60	
Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln 65 70 75 80	
Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr 85 90 95	
Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr 100 105 110	
Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe 115 120 125	

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg 145 . 150 155 160

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr

135

130

Arg	Ile	Lys	Ala	Ile 165	Ile	Val	Thr	Val	Trp 170	Val	Ile	Ser	Ala		Ile
				103					170					175	
Ser	Phe	Pro	Pro 180	Leu	Ile	Ser	Ile	Glu 185	rys	Lys	Gly	Ala	Gly 190	Gly	Gly
Gln	Gln	Pro 195	Ala	Glu	Pro	Ser	Cys 200	Lys	Ile	Asn	Asp	Gln 205	Lys	Trp	Tyŗ
Val	Ile 210	Ser	Ser	Ser	Ile	Gly 215	Ser	Phe	Phe _.	Ala	Pro 220	Cys	Leu	Ile	Met
Ile 225	Leu	Val	Tyr	Val	Arg 230	Ile	Tyr	Gln	Ile	Ala 235	Lys	Arg	Arg	Thr	Arg 240
Val	Pro	Pro	Ser	Arg 245	Arg	Gly	Pro	Asp	Ala 250	Cys	Ser	Ala	Pro	Pro 255	Gly
Gly	Ala	Asp	Arg 260	Arg	Pro	Asn	Gly	Leu 265	Gly	Pro	Glu	Arg	Gly 270	Ala	Gly
Pro	Thr	Gly 275	Ala	Glu	Ala	Glu	Pro 280	Leu	Pro	Thr	Gln	Leu 285	Asn	Gly	Ala
Pro	Gly 290	Glu	Pro	Ala	Pro	Ala 295	Gly	Pro	Arg	Asp ·	Gly 300	Asp	Ala	Leu	Asp
Leu 305	Glu	Glu	Ser	Ser	Ser 310	Ser	Glu	His	Ala	Glu 315	Arg	Pro	Pro	Gly	Pro 320
Arg	Arg	Pro	Asp	Arg 325	Gly	Pro	Arg	Ala	Lys 330	Gly	Lys	Thr	Arg	Ala 335	Ser
Gln	Val	Lys	Pro 340	Gly	Asp	Ser	Leu	Pro 345	Arg	Arg	Gly	Pro	Gly 350	Ala	Ala
Gly	Pro	Gly 355	Ala	Ser	Gly	Ser	Gly 360	His	Gly	Glu	Glu	Arg 365	Gly	Gly	Gly
Ala	Lys 370	Ala	Ser	Arg	Trp	Arg 375	Gly	Arg	Gln	Asn	Arg 380	Glu	Lys	Arg	Phe
Thr	Phe	Val	Leu	Ala	Vaļ	Val	Ile	Gly	Val	Phe	Val	Val	Суз	Trp	Phe

4/66

385 390 395 400

Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val Gly Cys Pro Val Pro 405 410 415

Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly Tyr Cys Asn Ser Ser 420 425 430

Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala 435 440 445

Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg Ile Val 450 455 460

<210> 3

<211> 1785

<212> DNA

<213> homo sapiens

<400> 3.

atggggaccg cccggatcgc acccggcctg gcgctcctgc tctgctgccc cgtgctcagc 60 teegegtacg egetggtgga tgeagatgac gteatgacta aagaggaaca gatetteetg 120 ctgcaccgtg ctcaggccca gtgcgaaaaa cggctcaagg aggtcctgca gaggccagcc 180 agcataatgg aatcagacaa gggatggaca tetgegteca catcagggaa geecaggaaa 240 300 gataaggcat ctgggaagct ctaccctgag tctgaggagg acaaggaggc acccactggc agcaggtacc gagggegeee etgtetgeeg gaatgggace acatectgtg etggeegetg 360 ggggcaccag gtgaggtggt ggctgtgccc tgtccggact acatttatga cttcaatcac 420 aaaggccatg cctaccgacg ctgtgaccgc aatggcagct gggagctggt gcctgggcac 480 aacaggacgt gggccaacta cagcgagtgt gtcaaatttc tcaccaatga gactcgtgaa 540 egggaggtgt ttgacegect gggcatgatt tacacegtgg getactcegt gteectggeg 600 teceteaceg tagetgtget cateetggee taetttagge ggetgeactg caegegeaac 660 tacatccaca tgcacctgtt cctgtccttc atgctgcgcg ccgtgagcat cttcgtcaag 720 gacgctgtgc tctactctgg cgccacgctt gatgaggctg agcgcctcac cgaggaggag 780 etgegegeea tegeceagge geeceegeeg eetgecaeeg eegetgeegg etaegeggge 840 900 tgcagggtgg ctgtgacctt cttcctttac ttcctggcca ccaactacta ctggattctg gtggagggc tgtacctgca cagcctcatc ttcatggcct tcttctcaga gaagaagtac 960 etgtgggget teacagtett eggetggggt etgeeegetg tettegtgge tgtgtgggte 1020

5/66

agtgtcagag	ctaccctggc	caacaccggg	tgctgggact	tgagctccgg	gaacaaaaag	1080
tggatcatcc	aggtgcccat	cctggcctcc	attgtgctca	acttcatcct	cttcatcaat	1140
atcgtccggg	tgctcgccac	caagctgcgg	gagaccaacg	ccggccggtg	tgacacacgg	1200
cagcagtacc	ggaagctgct	caaatccacg	ctggtgctca	tgcccctctt	tggcgtccac	1260
tacattgtct	tcatggccac	accatacacc	gaggtctcag	ggacgctctg	gcaagtccag	1320
atgcactatg	agatgctctt	caactccttc	cagggatttt	ttgtcgcaat	catatactgt	1380
ttctgcaatg	gcgaggtaca	agctgagatc	aagaaatctt	ggagccgctg	gacactggca	1440
ctggacttca	agcgaaaggc	acgcagcggg	agcagcagct	atagctacgg	ccccatggtg	1500
tcccacacaa	gtgtgaccaa	tgtcggcccc	cgtgtgggac	teggeetgee	cctcagcccc	1560
cgcctactgc	ccactgccac	caccaacggc	caccctcagc	tgcctggcca	tgccaagcca	1620
gggaccccag	ccctggagac	cctcgagacc	acaccacctg	ccatggctgc	tcccaaggac	1680
gatgggttcc	tcaacggctc	ctgctcaggc	ctggacgagg	aggcctctgg	gcctgagcgg	1740
ccacctgccc	tgctacagga	agagtgggag	acagtcatgt	gatga		1785

<210> 4

<211> 593

<212> PRT

<213> homo sapiens

<400> 4

Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys 1 5 10 15

Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met 20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys 35 40 45

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu 50 55 60

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys 65 70 75 80

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu 85 90 95 .

· Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

			100					105					110		
Asp	His	Ile 115	Leu	Cys	Trp	Pro	Leu 120	Gly	Ala	Pro	Gly	Glu 125	Val	Val	Ala
Val	Pro 130	Cys	Pro	Asp	Tyr	Ile 135	Tyr	Asp	Phe	Asn	His 140	Lys	Gly	His	Ala
Tyr 145	Arg	Arg	Cys	Asp	Arg 150	Asn	Gly	Ser	Trp	Glu 155	Leu	Val	Pro	Gļy	His 160
Asn	Arg	Thr	Trp	Ala 165	Asn	Tyr	Ser	Glu	Cys 170	Val	Lys	Phe	Leu	Thr 175	Asn
Glu	Thr	Arg	Glu 180	Arg	Glu	Val	Phe	Asp 185	Arg	Leu	Gly	Met	Ile 190	Туг	Thr
Val	Gly	Tyr 195	Ser	Val	Ser	Leu	Ala 200	Ser	Leu	Thr	Val	Ala 205	Val	Leu	Ile
Leu	Ala 210	Tyr	Phe	Arg	Arg	Leu 215	His	Cys	Thr	Arg	Asn 220	Tyr	Ile	His	Met
His 225		Phe	Leu	Ser	Phe 230	Met	Leu	Arg	Ala	Val 235	Ser	Ile	Phe	Val	Lys 240
Asp	Ala	Val	Leu	Tyr 245		Gly	Ala	Thr	Leu 250	Asp	Glu	Ala	Glu	Arg 255	Leu
Thr	Glu	Glu	Glu 260		Arg	Ala	Ile	Ala 265		Ala	Pro	Pro	Pro 270	Pro	Ala
Thr	Ala	Ala 275		Gly	Tyr	Ala	Gly 280		Arg	Val	Ala	Val 285	Thr	Phe	Phe
Leu	1 Tyr 290		. Leu	Ala	Thr	Asn 295		Tyr	Trp	Ile	Leu 300		Glu	Gly	Leu
Туг 305		His	s Ser	Leu	Ile 310		Met	. Ala	Phe	Phe 315		Glu	Lys	Lys	320
Leu	ı Trp	Gl ₃	y Phe	Thr 325		. Phe	e Gly	Trp	330 330		Pro	Ala	. Val	. Phe 335	val

Ala	Val	Trp	Val 340	Ser	Val	Arg	Ala	Thr 345	Leu	Ala	Asn	Thr	Gly 350	Cys	Trp
Asp	Leu	Ser 355	Ser	Gly	Asn	Lys	Lys 360	Trp	Ile	Ile	Gln	Val 365	Pro	Ile	Leu
Ala	Ser 370	Ile	Val	Ļeu	Asn	Phe 375	Ile	Leu	Phe	Ile	Asn 380	Ile	Val	Arg	Val
Leu 385	Ala	Thr	Lys	Leu	Arg 390	Glu	Thr	Asn	Ala	Gly 395	Arg	Cys ·	Asp	Thr	Arg 400
Gln	Gln	Tyr	Arg	Lys 405	Leu	Leu	Lys	Ser	Thr 410	Leu	Val	Leu	Met	Pro 415	Leu
Phe	Gly	Val	His 420	Tyr	Ile	Val	Phe	Met 425	Ala	Thr	Pro	Tyr	Thr 430	Glu	Val
Ser	Gly	Thr 435	Leu	Trp	Gln	Val	Gln 440	Met	His	Tyr	Glu	Met 445	Leu	Phe	Asn
Ser	Phe 450	Gln	Gly	Phe	Phe	Val 455	Ala	Ile	Ile	Tyr	Cys 460	Phe	Суз	Asn	Gly
Glu 465	Val	Gln	Ala	Glu	Ile 470	Lys	Lys	Ser	Trp	Ser 475	Arg	Trp	Thr	Leu	Ala 480
Ļeu	Asp	Phe	Lys	Arg 485	Lys	Ala	Arg	Ser	Gly 490	Ser	Ser	Ser	Tyr	Ser 495	Tyr
Gly	Pro	Met	Val 500	Ser	His	Thr	Ser	Val 505	Thr	Asn	Val	Gly	Pro 510	Arg	Val
Gly	Leu	Gly 515	Leu	Pro	Leu	Ser	Pro 520		Leu	Leu	Pro	Thr 525	Ala	Thr	Thr
Asn	Gly 530	His	Pro	Gln	Leu	Pro 535		His	Ala	Lys	Pro 540		Thr	Pro	Ala
Leu 545		Thr	Leu	Glu	Thr 550		Pro	Pro	Ala	Met 555		Ala	Pro	Lys	Asp 560
Asp	Gly	Phe	Leu	Asn 565		Ser	Суз	Ser	Gly 570		Asp	Glu	. Glu	Ala 575	

8/66

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val 580 585 590

Met

<210>

<211> 1238 <212> DNA homo sapiens <213> <400> 5 60 atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc 120 180 accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 240 qcctgcttcg tcctggtcct cacgcagagc tccatcttca gtctcctggc catcgccatt 300 360 qaccqctaca ttqccatccq catcccqctc cggtacaatg gcttggtgac cggcacgagg 420 gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg 480 540 qaqqqccaaq tqqcctqtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc 600 aacttettte etgtgtgetg gtgeecetge tgeteatget gggtgtetat ttgeggatet tectggegge gegacgaeag etgaageaga tggagageea geetetgeeg ggggageggg 660 cacggtccac actgcagaag gaggtccatg ctgccaagtc actggccatc attgtggggc 720 780 tetttgeeet etgetggetg eccetacaea teatcaactg etteaettte ttetgeeeeg 840 actgcagcca egecectete tggeteatgt acetggeeat egteetetee cacaccaatt 900 cggttgtgaa tcccttcatc tacgcctacc gtatccgcga gttccgccag accttccgca 960 agatcattcg cagccacgtc ctgaggcagc aagaaccttt caaggcagct ggcaccagtg cccgggtctt ggcagctcat ggcagtgacg gagagcaggt cagcctccgt ctcaacggcc 1020 1080 accegecagg agtgtgggee aaeggeagtg etececacee tgageggagg eccaatgget 1140 atgccctggg gctggtgagt ggagggagtg cccaagagtc ccaggggaac acgggcctcc 1200 cagacgtgga gctccttagc catgagctca agggagtgtg cccagagccc cctggcctag atgacccct ggcccaggat ggagcaggag tgtcctga 1238

<210> 6

9/66

<2	1	1	>	3	9	1

<212> PRT

<213> homo sapiens

<400> 6

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile 1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp 20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr 50 55 60

Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala 65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala 85 90 95

Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn 100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp 115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn 130 135 140

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu 145 150 155 160

Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met 165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Met 180 185 190

Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys 195 200 205

Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr Leu

10/66

210 215 220 Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly Leu 225 230 Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr Phe 245 Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu Ala 260 Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr Ala 275 Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser His Val Leu Arg Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg Leu Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His Pro Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly 355 Ser Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu 375 Leu Ser His Glu Leu Lys Gly <210> 7 <211> 720 <212> DNA <213> artificial sequence <220> <223> eCFP (enhanced CFP) cDNA sequence <400> 7 atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac.

ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac

60

120 ·

PCT/EP2003/014679 WO 2004/057333

11/66

ggcaagctga ccctg	aagtt catctgca	acc accggcaagc	tgcccgtgcc ctggc	ccacc 180
ctcgtgacca ccctg	acctg gggcgtgd	cag tgcttcagcc	gctaccccga ccaca	tgaag 240
cagcacgact tcttc	aagtc cgccatgo	ccc gaaggctacg	tccaggagcg cacca	tcttc 300
ttcaaggacg acggc	aacta caagacco	ege geegaggtga	agttcgaggg cgaca	ccctg 360
gtgaaccgca tcgag	ctgaa gggcatco	gac ttcaaggagg	acggcaacat cctgg	ggcac 420
aagctggagt acaac	tacat cagccaca	aac gtctatatca	ccgccgacaa gcaga	agaac 480
ggcatcaagg ccaac	ttcaa gatccgc	cac aacatcgagg	acggcagcgt gcago	tegee 540
gaccactacc agcag	aacac ccccatco	ggc gacggccccg	tgctgctgcc cgaca	accac 600
tacctgagca cccag	tccgc cctgagca	aaa gaccccaacg	agaagegega teaca	itggtc 660
ctgctggagt tcgtg	accgc cgccggga	atc actctcggca	tggacgagct gtaca	agtaa 720
<220> <223> eCFP (enh		ino acid seque eu Phe Thr Gly	Val Val Pro Ile	Leu
1	5	10	15	
Val Glu Leu Asp 20	Gly Asp Val A	sn Gly His Lys 25	Phe Ser Val Ser 30	Gly
Glu Gly Glu Gly 35		yr Gly Lys Leu O	Thr Leu Lys Phe 45	Ile
Cys Thr Thr Gly 50	Lys Leu Pro V 55	'al Pro Trp Pro	Thr Leu Val Thr 60	Thr
Leu Thr Trp Gly 65	Val Gln Cys P 70	he Ser Arg Tyr 75	Pro Asp His Met	Lys 80
Gln His Asp Phe	Phe Lvs Ser A	Ala Met Pro Glu	Gly Tyr Val Gln	Glu

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160	
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 225 230 235	
<210> 9 <211> 720 <212> DNA <213> artificial sequence	
<220> <223> YFP cDNA sequence	
<400> 9 atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac	60
ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac	120
ggcaagetga ceetgaagtt catetgeace aceggcaage tgeeegtgee etggeeeace	180
ctcgtgacca ccttcggcta cggcctgcag tgcttcgccc gctaccccga ccacatgaag	240
cagcacgact tettcaagte egecatgeee gaaggetaeg tecaggageg caccatette	300
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac	480
ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc	540

600

660

720

13/66

gaccactace ago	agaacac cccca	tegge gaeggeeeeg	tactactacc ca	acaaccac
	_	gcaaa gaccccaacg		
	- · ·	ggate acteteggea		
	regacege egeeg	ggace acceedgea	eggaegagee ge	acaaytaa
<210> 10 <211> 239 <212> PRT <213> artific	cial sequence			
<220> <223> YFP am	ino acid seque	nce		
<400> 10				
Met Val Ser Ly 1	ys Gly Glu Glu 5	Leu Phe Thr Gly 10		le Leu .5
Val Glu Leu As 20		Asn Gly His Lys 25	Phe Ser Val S	Ger Gly
Glu Gly Glu G. 35	ly Asp Ala Thr	Tyr Gly Lys Leu 40	Thr Leu Lys F	Phe Ile
Cys Thr Thr G	ly Lys Leu Pro 55	Val Pro Trp Pro	Thr Leu Val 1	Thr Thr
Phe Gly Tyr G	ly Leu Gln Cys 70	s Phe Ala Arg Tyr 75	Pro Asp His N	Met Lys 80
Gln His Asp P	he Phe Lys Ser 85	: Ala Met Pro Glu 90 .		Gln Glu 95
_	he Phe Lys Asr 00	o Asp Gly Asn Tyr 105	Lys Thr Arg 1	Ala Glu
Val Lys Phe G 115	lu Gly Asp Thi	r Leu Val Asn Arg 120	Ile Glu Leu 1 125	Lys Gly
Ile Asp Phe L 130	ys Glu Asp Gly 139	y Asn Ile Leu Gly 5	His Lys Leu (140	Glu Tyr
Asn Tyr Asn S 145	er His Asn Vai 150	l Tyr Ile Met Ala 155		Lys Asn 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

14/66

175 170 165 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 230 <210> 11 2457 . <211> <212> DNA artificial sequence <213> <220> alpha2a adrenergic receptor-cam cDNA sequence <223> <400> atgggctacc catacgacgt cccagactac gccagcatgg gctcactgca gccggatgcc 60 ggcaacagca gctggaacgg gaccgaagcg cccggaggcg gcacccgagc caccccttac 120 180 tecetgeagg tgacactgae getggtttge etggetggee tgeteatget gtteacagta 240 tttggcaacg tgctggttat tatcgcggtg ttcaccagtc gcgcgctcaa agctccccaa 300 aacctcttcc tggtgtccct ggcctcagcg gacatcctgg tggccacgct ggtcattccc ttttctttgg ccaacgaggt tatgggttac tggtactttg gtaaggtgtg gtgtgagatc 360 tatttggctc tcgacgtgct cttttgcacg tcgtccatag tgcacctgtg cgccatcagc 420 cttgaccgct actggtccat cacgcaggcc atcgagtaca acctgaagcg cacgccgcgt 480 cgcatcaagg ccatcattgt caccgtgtgg gtcatctcgg ctgtcatctc cttcccgcca 540 ctcatctcca tagagaagaa gggcgctggc ggcgggcagc agccggccga gccaagctgc 600 aagatcaacg accagaagtg gtatgtcatc tectegteea teggtteett ettegegeet 660 tgcctcatca tgatcctggt ctacgtgcgt atttaccaga tcgccaagcg tcgcacccgc 720 780 gtgcctccca gccgccgggg tccggacgcc atggtgagca agggcgagga gctgttcacc 840 ggggtggtgc ccatcctggt cgagctggac ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac ggcaagctga ccctgaagtt catctgcacc 900

accggcaage tgcccgtgcc ctggcccacc ctcgtgacca ccttcggcta cggcctgcag

960

tgcttcgccc	gctaccccga	ccacatgaag	cagcacgact	tcttcaagtc	cgccatgccc	1020
gaaggctacg	tccaggagcg	caccatcttc	ttcaaggacg	acggcaacta	caagacccgc	1080
gccgaggtga	agttcgaggg	cgacaccctg	gtgaaccgca	tcgagctgaa	gggcatcgac	1140
ttcaaggagg	acggcaacat	cctggggcac	aagctggagt	acaactacaa	cagccacaac	1200
gtctatatca	tggccgacaa	gcagaagaac	ggcatcaagg	tgaacttcaa	gatccgccac	1260
aacatcgagg	acggcagcgt	gcagctcgcc	gaccactacc	agcagaacac	ccccatcggc	1320
gacggccccg	tgctgctgcc	cgacaaccac	tacctgagct	accagtccgc	cctgagcaaa	1380
gaccccaacg	agaagcgcga	tcacatggtc	ctgctggagt	tcgtgaccgc	cgccgggatc	1440
actctcggca	tggacgagct	gtacaagcgc	tggcgcggga	ggcaaaaccg	ggagaaacgc	1500
ttcacgttcg	tgctggcggt	ggtgatcggc	gtgttcgtgg	tgtgttggtt	tccgttcttt	1560
ttcacctaca	cgctcatagc	ggtcggctgc	ccggtgccca	gccagctctt	caacttcttc	1620
ttctggttcg	gctactgcaa	cagctcgctg	aaccctgtta	tctacaccat	cttcaaccac	1680
gacttccgac	gcgccttcaa	gaagatcctc	tgccgtgggg	acagaaaacg	catcgtgatg	1740
gtgagcaagg	gcgaggagct	gttcaccggg	gtggtgccca	tcctggt:cga	gctggacggc	1800
gacgtaaacg	gccacaagtt	cagcgtgtcc	ggcgagggcg	agggcgatgc	cacctacggc	1860
aagctgaccc	tgaagttcat	ctgcaccacc	ggcaagctgc	ccgtgccctg	gcccaccctc	1920
gtgaccaccc	tgacctgggg	cgtgcagtgc	ttcagccgct	accccgacca	catgaagcag	1980
cacgacttct	tcaagtccgc	catgcccgaa	ggctacgtcc	aggagcgcac	catcttcttc	2040
aaggacgacg	gcaactacaa	gacccgcgcc	gaggtgaagt	tcgagggcga	caccctggtg	2100
aaccgcatcg	agctgaaggg	catcgacttc	aaggaggacg	gcaacatcct	ggggcacaag	2160
ctggagtaca	actacatcag	ccacaacgtc	tatatcaccg	ccgacaagca	gaagaacggc	2220
atcaaggcca	acttcaagat	ccgccacaac	atcgaggacg	gcagcgtgca	gctcgccgac	2280
cactaccago	agaacacccc	catcggcgac	ggccccgtgc	tgctgcccga	caaccactac	2340
ctgagcaccc	agtccgccct	gagcaaagac	cccaacgaga	agcgcgatca	catggtcctg	2400
ctggagttcg	tgaccgccgc	cgggatcact	ctcggcatgg	acgagctgta	caagtaa	2457

<210> 12 <211> 818 <212> PRT <213> artificial sequence

<220>

<223> alpha 2a adrenergic receptor-cam "chameleon" amino acid sequence

16/66

< 4	0	0>	1:	2

Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Met Gly Ser Leu 1 5 10 15

Gln Pro Asp Ala Gly Asn Ser Ser Trp Asn Gly Thr Glu Ala Pro Gly 20 25 30

Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu 35 40 45 .

Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val 50 55 60

Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln 65 70 75 80

Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr 85 90 95

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
100 105 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe 115 120 . 125

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr 130 135 140

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg 145 150 155 160

Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile 165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly 180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr 195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met 210 215 220

Ile 225	Leu	Val	Tyr	Val	Arg 230	Ile	Tyr	Gln	Ile	Ala 235	Lys	Arg	Arg	Thr	Arg 240
Val	Pro	Pro	Ser	Arg 245	Arg	Gly	Pro	Asp	Ala 250	Met	Val	Ser	Lys	Gly 255	Glu
Glu	Leu	Phe	Thr 260	Gly	Val	Val	Pro	Ile 265	Leu	Val	Glu	Leu	Asp 270	Gly	Asp
Val	Asn	Gly 275	His	Lys	Phe	Ser	Val 280	Ser	Gly	Glu	Gly	Glu 285	Gly	Asp	Ala
Thr	Tyr 290	Gly	Lys	Leu	Thr	Leu 295	Lys	Phe	Ile	Cys	Thr 300	Thr	Gly	Lys	Leu
Pro 305	Val	Pro	Trp	Pro	Thr 310	Leu	Val	Thr	Thr	Phe 315	Gly	Tyr	Gly	Leu	Gln 320
Cys	Phe	Ala	Arg	Tyr 325	Pro	Asp	His	Met	Lys 330	Gln	His	Asp	Phe	Phe 335	Lys
Ser	Ala	Met	Pro 340	Glu	Gly	Tyr	Val	Gln 345	Glu	Arg	Thr	Ile	Phe 350	Phe	Lys
Asp	Asp	Gly 355	Asn	Tyr	Lys	Thr	Arg 360	Ala	Glu	Val	Lys	Phe 365	Glu	Gly	Asp
Thr	Leu 370	Val	Asn	Arg	Ile	Glu 375	Leu	ГÀЗ	Gly	Ile	Asp 380	Phe	Lys	Glu	Asp
Gly 385	Asn	Ile	Leu	Gly		Lys		Glu	Tyr		Tyr		Ser		Asn 400
Val	Tyr	Ile	Met	Ala 405	Asp	Lys	Gln	Lys	Asn 410	Gly	Ile	Lys	Val	Asn 415	Phe
Lys	Ile	Arg	His 420	Asn	Ile	Glu	Asp	Gly 425	Ser	Val	Gln	Leu	Ala 430	Asp	His
Tyr	Gln	Gln 435	Asn	Thr	Pro	Ile	Gly 440	Asp	Gly	Pro	Val	Leu 445	Leu	Pro	Asp
Asn	His 450		Leu	Ser	Tyr	Gln 455		Ala	Leu	Ser	Lys 460		Pro	Asn	Glu

Lys 465	Arg	Asp	His	Met	Val 470	Leu	Leu	Glu	Phe	Val 475	Thr	Ala	Ala	Gly	Ile 480
Thr	Leu	Gly	Met	Asp 485	Glu	Leu	Tyr	Lys	Arg 490	Trp	Arg	Gly	Arg	Gln 495	Asn
Arg	Glu	Lys	Arg 500	Phe	Thr	Phe	Val	Leu 505	Ala	Val	Val	Ile	Gly 510	Val	Phe
Val	Val	Cys 515	Trp	Phe	Pro	Phe	Phe 520	Phe	Thr	Tyr	Thr	Leu 525	Ile	Ala	Val
Gly	Cys 530	Pro	Val	Pro	Ser	Gln 535	Leu	Phe	Asn	Phe	Phe 540	Phe	Trp	Phe	Gly
Tyr 545	Cys	Asn	Ser	Ser	Leu 550	Asn	Pro	Val	Ile	Tyr 555	Thr	Ile	Phe	Asn	His 560
Asp	Phe	Arg	Arg	Ala 565	Phe	Lys	Lys	Ile	Leu 570	Cys	Arg	Gly	Asp	Arg 575	Lys
Arg	Ile	Val	Met 580	Val	Ser	Lys	Gly	Glu 585	Glu	Leu	Phe	Thr	Gly 590	Val	Val
Pro	Ile	Leu 595	Val	Glu	Leu	Asp	Gly 600	Asp	Val	Asn	Gly	His 605	Lys	Phe	Ser
Val	Ser 610	Gly	Glu	GŢY	Glu	Gly 615	Asp	Ala	Thr	Tyr	Gly 620		Leu	Thr	Leu
Lys 625		Ile	Cys	Thr	Thr 630		Lys	Leu	Pro	Val 635		Trp	Pro	Thr	Leu 640
Val	Thr	Thr	Leu	Thr 645		Gly ·	Val	Gln	Cýs 650		Ser	Arg	Tyr	Pro 655	Asp
His	Met	. Lys	Gln 660		Asp	Phe	Phe	Lys 665		Àla	Met	Pro	670		Tyr
Val	Gln	Glu 675		Thr	: Ile	Phe	Phe 680		a Asp	Asp	Gly	Asr 685	ı Tyr	Lys	Thr
Arg	Ala		ı Val	. Lys	s Phe	Glu		/ Asp	Thi	: Leu	ı Val		n Arg	, Ile	Glu

Leu 1705	Lys	Gly	Ile	Asp	Phe 710	Lys	Glu	Asp	Gly	Asn 715	Ile	Leu	Gly	His	Lys 720	
Leu (Glu	Tyr	Asn	Tyr 725	Ile	Ser	His	Asn	Val 730	Tyr	Ile	Thr	Ala	Asp 735	Lys	
Gln :	Lys	Asn	Gly 740	Ile	Lys ·	Ala	Asn	Phe 745	Lys	Ile	Arg	His	Asn 750	Ile	Glu	
Asp	Gly	Ser 755	Val	Gln	Leu	Ala	Asp 760	His	Tyr	Gln	Gln	Asn 765	Thr	Pro	Ile	
Gly .	Asp 770	Gly	Pro	Val	Leu	Leu 775	Pro	Asp	Asn	His	Tyr 780	Leu	Ser	Thr	Gln	
Ser 785	Ala	Leu	Ser	Lys	Asp 790	Pro	Asn	Glu	Lys	Arg 795	Asp	His	Met	Val	Leu 800	
Leu	Glu	Phe	Val	Thr 805	Ala	Ala	Gly	Ile	Ţhr 810	Leu	Gly	Met	Asp	Glu 815	Leu	
Tyr	Lys															
<211 <212	<210> 13 <211> 2928 <212> DNA <213> artificial sequence															
<220 <223		PTH	rece	ptor	-can	"ch	amel.	eon"	8 c	DNA	sequ	ence	1			
<400 atgg)> ggga	13 .ccg	cccg	gato	gc a	cccg	gcct	g go	gctc	ctgo	tct:	gctç	lccc	cgtç	etcagc	60
tcc	gcgt	acg	cgct	ggtç	ıga t	gcag	atga	c gt	catg	gacta	aag	gagga	aca	gato	ttcctg	120
ctg	cacc	gtg	ctca	ggcc	ca ç	tgcg	jaaaa	a c	gcto	aagg	g ago	gtcct	:gca	gago	gecagee	180
agca	ataa	tgg	aato	agac	aa q	ggat	ggad	ca to	etgeg	gtcca	cat	cago	ggaa	gcco	caggaaa	240
gata	aagg	gcat	ctg	gaaq	jct d	ctaco	ctga	ag to	ctgag	ggagg	g aca	aagga	aggc	acco	cactggc	300
agc	aggt	acc	gagg	ggcgo	cc o	etgto	etge	eg ga	aatgg	ggaco	aca	atcct	gtg	ctg	geegetg	360
ggg	gcad	ccag	gtga	aggt	ggt (gct	gtgco	ec to	gtcc	ggact	aca	attta	atga	ctt	caatcac	420
aaa	ggco	catg	ccta	accga	acg (ctgt	gacc	gc a	atggo	cagct	t gg	gagc	tggt	gcct	tgggcac	480

aacaggacgt	gggccaacta	cagcgagtgt	gtcaaatttc	tcaccaatga	gactcgtgaa	540
cgggaggtgt	ttgaccgcct	gggcatgatt	tacaccgtgg	gctactccgt	gtccctggcg	600
tccctcaccg	tagctgtgct	catcctggcc	tactttaggc	ggctgcactg	cacgcgcaac	660
tacatccaca	tgcacctgtt	cctgtccttc	atgctgcgcg	ccgtgagcat	cttcgtcaag	720
gacgctgtgc	tctactctgg	cgccacgctt	gatgaggctg	agcgcctcac	cgaggaggag	780
ctgcgcgcca	tcgcccaggc	gccccgccg	cctgccaccg	ccgctgccgg	ctacgcgggc	840
tgcagggtgg	ctgtgacctt	cttcctttac	ttcctggcca	ccaactacta	ctggattctg	900
gtggaggggc	tgtacctgca	cagcctcatc	ttcatggcct	tcttctcaga	gaagaagtac	960
ctgtggggct	tcacagtctt	cggctggggt	ctgcccgctg	tcttcgtggc	tgtgtgggtc	1020
agtgtcagag	ctaccctggc	caacaccggg	tgctgggact	tgagctccgg	gaacaaaaag	1080
tggatcatcc	aggtgcccat	cctggcctcc	attgtgctca	acttcatcct	cttcatcaat	1140
atcgtccggg	tgctcgccac	caagctgcgg	gagaccaacg	ccggcatggt	gagcaagggc	1200
gaggagctgt	tcaccggggt	ggtgcccatc	ctggtcgagc	tggacggcga	cgtaaacggc	1260
cacaagttca	gcgtgtccgg	cgagggcgag	ggcgatgcca	cctacggcaa	gctgaccctg	1320
aagttcatct	gcaccaccgg	caagctgccc	gtgccctggc	ccaccctcgt	gaccaccctg	1380
acctggggcg	tgcagtgctt	cagccgctac	cccgaccaca	tgaagcagca	cgacttcttc	1440
aagtccgcca	tgcccgaagg	ctacgtccag	gagcgcacca	tcttcttcaa	ggacgacggc	1500
aactacaaga	cccgcgccga	ggtgaagttc	gagggcgaca	ccctggtgaa	ccgcatcgag	1560
ctgaagggca	tcgacttcaa	ggaggacggc	aacatcctgg	ggcacaagct	ggagtacaac	1620
tacatcagcc	acaacgtcta	tatcaccgcc	gacaagcaga	agaacggcat	caaggccaac	1680
ttcaagatcc	gccacaacat	cgaggacggc	agcgtgcagc	tcgccgacca	ctaccagcag	1740
aacaccccca	tcggcgacgg	ccccgtgctg	ctgcccgaca	accactacct	gagcacccag	1800
tccgccctga	gcaaagaccc	caacgagaag	cgcgatcaca	tggt.cctgct	ggagttcgtg	1860
accgccgccg	ggatcactct	cggcatggac	gagctgtaca	agcggtgtga	cacacggcag	1920
cagtaccgga	agctgctcaa	atccacgctg	gtgctcatgc	ccctctttgg	cgtccactac	1980
attgtcttca	tggccacacc	atacaccgag	gtctcaggga	cgctctggca	agtccagatg	2040
cactatgaga	tgctcttcaa	ctccttccag	ggatttttg	tcgcaatcat	atactgtttc	2100
tgcaatggcg	aggtacaagc	tgagatcaag	aaatcttgga	gccgctggac	actggcactg	2160
gacttcaagc	gaaaggcacg	cagcgggagc	agcagctata	gctacggcat	ggtgagcaag	2220
ggcgaggagc	tgttcaccgg	ggtggtgccc	atcctggtcg	agctggacgg	cgacgtaaac	2280

21/66

ggccacaagt tcagcgtgtc cggcgagggc gagggcgatg ccacctacgg caag	getgace 2340
ctgaagttca tctgcaccac cggcaagctg cccgtgccct ggcccaccct cgtg	gaccacc 2400
tteggetacg geetgeagtg ettegeeege tacceegace acatgaagea geac	egacttc 2460
ttcaagtccg ccatgcccga aggctacgtc caggagcgca ccatcttctt caag	ggacgac 2520
ggcaactaca agacccgcgc cgaggtgaag ttcgagggcg acaccctggt gaac	ccgcatc 2580
gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacaa gctg	ggagtac 2640
aactacaaca gccacaacgt ctatatcatg gccgacaagc agaagaacgg catc	caaggtg 2700
aacttcaaga tccgccacaa catcgaggac ggcagcgtgc agctcgccga ccac	ctaccag 2760
cagaacaccc ccatcggcga cggccccgtg ctgctgcccg acaaccacta cctg	gagctac 2820
cagtccgccc tgagcaaaga ccccaacgag aagcgcgatc acatggtcct gctg	ggagttc 2880
gtgaccgccg ccgggatcac tctcggcatg gacgagctgt acaagtaa	2928

<210> 14

<211> 975

<212> PRT

<213> artificial sequence

<220>

<223> PTH receptor-cam8 "chameleon" amino acid sequence

<400> 14

Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys 1 10 15

Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Val Met 20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys 35 40 45

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu 50 55 60

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys 65 70 75 80

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu 85 90 . 95

Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

22/66

100 105 110 Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala 115 120 Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala 130 135 Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His 150 145 155 Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn . 165 170 Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr 185 Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu 250 Thr Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala 265 Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe 280 Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu 295 Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr 310 Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val 325 . 330 335

23/66

									23	700		•			
Ala	Val	Trp	Val 340	Ser	Val	Arg	Ala	Thr 345	Leu	Ala	Asn	Thr	Gly 350	Cys	Trp
Asp	Leu	Ser 355	Ser	Gly	Asn	Lys	Lys 360	Trp	Ile	Ile	Gln	Val 365	Pro	Ile	Leu
Ala	Ser 370	Ile	Val	Leu	Asn	Phe 375	Ile	Leu	Phe	Ile	Asn 380	Ile	Val	Arg	Val
Leu 385	Ala	Thr	Lys	Leu	Arg 390	Glu	Thr	Asn	Ala	Gly 395	Met	Val	Ser	Lys	Gly 400
Glu	Glu	Leu	Phe	Thr 405	Gly	Val	Val	Pro	Ile 410	Leu	Val	Glu	Leu	Asp 415	Gly
Asp	Val	Asn	Gly 420	His	Lys	Phe	Ser	Val 425	Ser	Gly	Glu	Gly	Glu 430	Gly	Asp
Ala	Thr	Tyr 435	Gly	Lys	Leu	Thr	Leu 440	Lys	Phe	Ile	Суз	Thr 445	Thr	Gly	Lys
Leu	Pro 450	Val	Pro	Trp	Pro	Thr 455	Leu	Val	Thr	Thr	Leu 460	Thr	Trp	Gly	Val
Gln 465		Phe	Ser	Arg	Tyr 470	Pro	Asp	His	Met	Lys 475	Gln	His	Asp	Phe	Phe 480
Lys	Ser	Ala	Met	Pro 485	Glu	Gly	Tyr	Val	Gln 490	Glu	Arg	Thr	Ile	Phe 495	Phe
Lys	Asp	Asp	Gly 500	Asn	Tyr	Lys	Thr	Arg 505	Ala	Glu	Val	Lys	Phe 510	Glu	Gly
Asp	Thr	Leu 515	Val	Asn	Arg	Ile	Glu 520	Leu	Lys	Gly	Ile	Asp 525	Phe	Ьys	Glu
Asp	Gly 530	Asn	Ile	Leu	Gly	His 535	Lys	Leu	Glu	Tyr	Asn 540	Tyr	Ile	Ser	His
Asn 545		Tyr	Ile	Thr	Ala 550	Asp	Lys	Gln	Lys	Asn 555	_	Ile	Lys	Ala	Asn 560
Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp

570

. 575

565

His	Tyr	Gln	Gln 580	Asn	Thr	Pro	Ile	Gly 585	Asp	Gly	Pro	Val	Leu 590	Leu	Pro
Asp	Asn	His 595	Tyr	Leu	Ser	Thr	Gln 600	Ser	Ala	Leu	Ser	Lys 605	Asp	Pro	Asn
Glu	Lys 610	_	Asp	His	Met	Val 615	Leu	Leu	Glu	Phe	Val 620	Thr	Ala	Ala	Gly
Ile 625	Thr	Leu	Gly	Met	Asp 630	Glu	Ĺeu	Tyr	Lys	Arg 635	Суѕ	'Asp	Thr	Arg	Gln 640
Gln	Tyr	Arg	Lys	Leu 645	Leu	Lys	Ser	Thr	Leu 650	Val	Leu	Met	Pro	Leu 655	Phe
Gly	Val	His	Tyr 660	Ile	Val	Phe	Met	Ala 665	Thr	Pro	Tyr	Thr	Glu 670	Val	Ser
Gly	Thr	Leu 675	Trp	Gln	Val		Met . 680	His	Tyr	Glu	Met	Leu 685	Phe	Asn	Ser
Phe	Gln 690	Gly	Phe	Phe	Val	Ala 695	Ile	Ile	Tyr	Суз	Phe 700	Cys	Asn	Gly	Glu
Val 705	Gln	Ala	Glu	Ile	Lys 710	Lys	Ser	Trp	Ser	Arg 715		Thr	Leu	Ala	Leu 720
Asp	Phe	Lys	Arg	Lys 725		Arg	Ser	Gly	Ser 730		Ser	Tyr	Ser	Tyr 735	Gly
Met	Val	Ser	Lys 740		Glu	Glu	Leu	Phe 745		Gly	Val	Val	Pro 750		Leu
Val	Glu	Leu 755		Gly	Asp	Val	Asn 760		His	Lys	Phe	Ser 765	Val	Ser	Gl
Glu	Gly 770		Gly	' Asp	Ala	Thr 775		Gly	, Lys	. Leu	Thr 780		ı Lys	Phe	. Ile
Cys 785		Thr	Gly	, Lys	790		Val	. Pro	Trp	795		: Let	ı Val	. Thr	Th:
Phe	e Gly	у Туг	: Gly	/ Lev		. Cys	B Phe	e Ala	a Arg 810	_	r Pro) Ası	o His	Met 815	

Gln	His	Asp	Phe 820	Phe	Lys	Ser	Ala	Met 825	Pro	Glu	Gly	Tyr	Val 830	Gln	Glu		
Arg	Thr	Ile 835	Phe	Phe	Lys	Asp	Asp 840	Gly	Asn	Tyr	Lys	Thr 845	Arg	Ala	Glu		
Val	Lys 850	Phe	Glu	Gly	Asp	Thr 855	Leu	Val	Asn	Arg	Ile 860	Glu	Leu	Lys	Gly		
Ile 865	Asp	Phe	Lys	Glu	Asp 870	Gly	Asn	Ile	Leu	Gly 875	His	Lys	Leu	Glu	Tyr 880		
Asn	Tyr	Asn	Ser	His 885	Asn	Val	Tyr	Ile	Met 890	Ala	Asp	Lys	Gln	Lys 895	Asn		
Gly	Ile	Lys	Val 900	Asn ·	Phe	Lys	Ile	Arg 905	His	Asn	Ile	Glu	Asp 910	Gly	Ser		
Val	Gln	Leu 915	Ala	Asp	His	Tyr	Gln 920	Gln	Asn	Thr	Pro	Ile 925	Gly	Asp	Gly		
Pro	Val 930	Leu	Leu	Pro	Asp	Asn 935	His	Tyr	Leu	Ser	Tyr 940	Gln	Ser	Ala	Leu		
Ser 945	Lys	Asp	Pro	Asn	Glu 950	Lys	Arg	Asp	His	Met 955		Leu	Leu	Glu	Phe 960		
Val	Thr	Ala	Ala	Gly 965		Thr	Leu	Gly	Met 970		Glu	Leu	Tyr	Lys 975			
<21 <21 <21 <21	1> 2>	15 2361 DNA arti	fici	al s	eque	nce											
<22 <22	-	A2A-	CFP1	4/10	-YFP	-C33	cDN	A se	quen	.ce;	A2A	"cha	mele	on"			
<40 atg		15 tca	tggg	ctcc	tc g	gtgt	acat	c ac	:ggtg	gago	tgg	rccat	tgc	tgtg	ctggcc	•	60
															paacgtc	1	20
acc	aact	act	ttgt	ggtg	tc a	ctgg	cggc	g gc	cgac	atcg	, cag	ıtggç	ıtgt	gcto	gccatc	1	.80
ccc	tttg	cca	tcac	cato	ag c	acco	Iggtt	c to	geget	gcct	gec	cacgo	gctg	ccto	ttcatt	2	40

gcctgcttcg	tcctggtcct	cacgcagagc	tccatcttca	gtctcctggc	catcgccatt	300
gaccgctaca	ttgccatccg	catcccgctc	cggtacaatg	gcttggtgac	cggcacgagg	360
gctaagggca	tcattgccat	ctgctgggtg	ctgtcgtttg	ccatcggcct	gactcccatg	420
ctaggttgga	acaactgcgg	tcagccaaag	gagggcaaga	accactccca	gggctgcggg	480
gagggccaag	tggcctgtct	ctttgaggat	gtggtcccca	tgaactacat	ggtgtacttc	540
aacttctttg	cctgtgtgct	ggtgcccctg	ctgctcatgc	tgggtgtcta	tttgcggatc	600
ttcctggcgg	cgcgacgaca	gctgaagcag	atggaggtga	gcaagggcga	ggagctgttc	660
accggggtgg	tgcccatcct	ggtcgagctg	gacggcgacg	taaacggcca	caagttcagc	720
gtgtccggcg	agggcgaggg	cgatgccacc	tacggcaagc	tgaccctgaa	gttcatctgc	780
accaccggca	agctgcccgt	gccctggccc	accctcgtga	ccaccctgac	ctggggcgtg	840
cagtgcttca	gccgctaccc	cgaccacatg	aagcagcacg	acttcttcaa	gtccgccatg	900
cccgaaggct	acgtccagga	gcgcaccatc	ttcttcaagg	acgacggcaa	ctacaagacc	960
cgcgccgagg	tgaagttcga	gggcgacacc	ctggtgaacc	gcatcgagct	gaagggcatc	1020
gacttcaagg	aggacggcaa	catcctgggg	cacaagctgg	agtacaacta	catcagccac	1080
aacgtctata	tcaccgccga	caagcagaag	aacggcatca	aggccaactt	caagatccgc	1140
cacaacatcg	aggacggcag	cgtgcagctc	gccgaccact	accagcagaa	cacccccatc	1200
ggcgacggcc	ccgtgctgct	gcccgacaac	cactacctga	gcacccagtc	cgccctgagc	1260
aaagacccca	acgagaagcg	cgatcacatg	gtcctgctgg	agttcgtgac	cgccgccggg	1320
atcactctcg	gcatggacga	gctgtacaag	cttcagaagg	aggtccatgc	tgccaagtca	1380
ctggccatca	ttgtggggct	ctttgccctc	tgctggctgc	ccctacacat	catcaactgc	1440
ttcactttct	tctgccccga	ctgcagccac	gcccctctct	ggctcatgta	cctggccatc	1500
gtcctctccc	acaccaattc	ggttgtgaat	cccttcatct	acgcctaccg	tatccgcgag	1560
ttccgccaga	ccttccgcaa	gatcattcgc	agccacgtcc	tgaggcagca	agaacctttc	1620
aaggcagctg	gcaccagtgc	cegggtegtg	agcaagggcg	aggagctgtt	caccggggtg	1680
gtgcccatcc	tggtcgagct	ggacggcgac	gtaaacggcc	acaagttcag	cgtgtccggc	1740
gagggcgagg	gcgatgccac	ctacggcaac	ctgaccctga	agttcatctg	caccaccggc	1800
aagctgcccg	tgccctggcc	caccctcgto	, accaccttcg	gctacggcct	gcagtgcttc	1860
gcccgctacc	ccgaccacat	gaagcagcac	gacttcttca	agtccgccat	gcccgaaggc	1920
tacgtccagg	agegeaceat	cttcttcaaq	g gacgacggca	actacaagac	ccgcgccgag	1980
gtgaagttcg	agggcgacac	cctggtgaad	c cgcatcgago	tgaagggcat	cgacttcaag	2040

27/66

gaggacggca acatectggg geacaagetg gagtacaaet acaacageca caacgtetat	2100
atcatggccg acaagcagaa gaacggcatc aaggtgaact tcaagatccg ccacaacatc	2160
gaggacggca gcgtgcagct cgccgaccac taccagcaga acacccccat cggcgacggc	2220
cccgtgctgc tgcccgacaa ccactacctg agctaccagt ccgccctgag caaagacccc	2280
aacgagaagc gcgatcacat ggtcctgctg gagttcgtga ccgccgccgg gatcactctc	2340
ggcatggacg agctgtacaa g	2361
<pre><210> 16 <211> 784 <212> PRT <213> artificial sequence <220> <223> A2A-CFP14/10-YFP-C33 amino acid sequence; "A2A chameleon"</pre>	
<400> 16	
Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile 1 5 10 15	
Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp 20 25 30	
Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala 35 40 45	
Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr 50 55 60	
Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala 65 70 75 80	
Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala 85 90 95	
Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn 100 105 110	

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn . 130 $$135\$

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp

120

115

Cys 145	Gly	Gln	Pro	Lys	Glu 150	Gly	Lys	Asn	His	Ser 155	Gln	Gly	Cys	Gly	Glu 160
Gly	Gln	Val	Ala	Cys 165	Leu	Phe	Glu	Asp	Val 170	Val	Pro	Met	Asn	Туг 175	Met
Val	Tyr	Phe	Asn 180	Phe	Phe	Ala	Cys	Val 185	Leu	Val	Pro	Leu	Leu 190	Leu	Met
Leu	Gly	Val 195	Tyr	Leu	Arg	Ile	Phe 200	Leu	Ala	Ala	Arg	Arg 205	Gln	Leu	ГÀЗ
Gln	Met 210	Glu	Val	Ser	Lys	Gly 215	Glu	Glu	Leu	Phe	Thr 220	Gly	Val	Val	Pro
Ile 225	Leu	Val	Glu	Leu	Asp 230	Gly	Asp	Val	Asn	Gly 235	His	Lys	Phe	Ser	Val 240
Ser	Gly	Glu	Gly	Glu 245	Gly	Asp	Ala	Thr	Tyr 250	Gly	Lys	Leu	Thr	Leu 255	Lys
Phe	Ile	Cys	Thr 260	Thr	Gly	Lys	Leu	Pro 265	Val	Pro	Trp	Pro	Thr 270	Leu	Val
Thr	Thr	Leu 275	Thr	Trp	Gly	Val	Gln 280	Суз	Phe	Ser	Arg	Tyŕ 285		Asp	His
Met	Lys 290	Gln	His	Asp	Phe	Phe 295		Ser	Ala	Met	Pro 300		Gly	Tyr	Val
Gln 305	Glu	Arg	Thr	Ile	Phe 310	Phe	Lys	Asp	Asp	Gly 315		Tyr	Lys	Thr	Arg 320
Ala	Glu	Val	Lys	Phe 325	Glu	Gly	Asp	Thr	330		Asn	Arg	, Ile	Glu 335	Lev
Lys	Gly	Ile	340		Lys	Glu	Asp	Gly 345		ı Ile	. Leu	ı Gly	7 His		: Lev
Glu	Tyr	Asn 355		Ile	: Ser	His	Asn 360		. Туг	: Ile	. Thr	365		Lys	Glr
Lys	Asn		, Ile	Lys	: Ala	Asr		e Lys	s Ile	arç	y His		ı Ile	e Glu	ı Ası

Gly 385	Ser	Val	Gln	Leu	Ala 390	Asp	His	Tyr		Gln 395	Asn	Thr	Pro		Gly 400
Asp	Gly	Pro	Val	Leu 405	Leu	Pro	Asp	Asn	His 410	Tyr	Leu	Ser	Thr	Gln 415	Ser
Ala	Leu	Ser	Lys 420	Asp	Pro	Asn	Glu	Lys 425	Arg	Asp	His	Met	Val 430	Leu	Leu
Glu	Phe	Val 435	Thr	Ala	Ala	Gly	Ile 440	Thr	Leu	Gly	Met	Asp 445	Glu	Leu	Tyr
Lys	Leu 450	Gln	Lys	Glu	Val	His 455	Ala	Ala	Lys	Ser	Leu 460	Ala	Ile	Ile	Val
Gly 465	Leu	Phe	Ala	Leu	Cys 470	Trp	Leu	Pro	Leu	His 475	Ile	Ile	Asn	Cys	Phe 480
Thr	Phe	Phe	Cys	Pro 485	Asp	Суз	Ser	His	Ala 490	Pro	Leu	Trp	Leu	Met 495	Tyr
Leu	Ala	Ile	Val 500	Leu	Ser	His	Thr	Asn 505	Ser	∀al	Val	Asn	Pro 510	Phe	Ile
Tyr	Ala	Tyr 515	Arg	Ile	Arg	Glu	Phe 520	Arg	Gln	Thr	Phe	Arg 525	Lys	Ile	Ile
Arg	Ser 530	His	Val	Leu	Arg	Gln 535	Gln	Glu	Pro	Phe	Lys 540	Ala	Ala	Gly	Thr
Ser 545	Ala	Arg	Val	Met	Val 550	Ser	Lys	Gly	Glu	Glu 555	Leu	Phe	Thr	Gly	Val 560
Val	Pro	Ile	Leu	Val 565		Leu	Asp	Gly	Asp 570		Asn	Gly	His	Lys 575	Phe
Ser	Val	Ser	Gly 580		Gly	Glu	Gly	Asp 585	Ala	Thr	Tyr	Gly	Lys 590	Leu	Thr
Leu	Lys	Phe 595		Cys	Thr	Thr	Gly 600		Leu	Pro	Val	Pro 605		Pro	Thr
Leu	Val	Thr	Thr	Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro

	610					615					620.						
Asp 625	His	Met	Lys	Gln	His 630	Asp	Phe	Phe	Lуs	Ser 635	Ala	Met	Pro	Glu	Gly 640		
Tyr	Val	Gln	Glu	Arg 645	Thr	Ile	Phe	Phe	Lys 650	Asp	Asp	Gly	Asn	Tyr 655	Lys		
Thr	Arg	Ala	Glu 660	Val	Lys	Phe	Glu	Gly 665	Asp	Thr	Leu	Val	Asn 670	Arg	Ile		
Glu	Leu	Lys 675	Gly	Ile	Asp	Phe	Lys 680	Glu	Asp	Gly	Asn	Ile 685	Leu	Gly	His		
Lys	Leu 690	Glu	Tyr	Asn	Tyr	Asn 695	Ser	His	Asn	Val	Tyr 700	Ile	Met	Ala	Asp		
Lys 705	Gln	Lys	Asn	Gly	Ile 710	Lys	Val	Asn	Phe	Lys 715	Ile	Arg	His	Asn	Ile 720		
Glu	Asp	Gly	Ser	Val 725	Gln	Leu	Ala	Asp	His 730	Tyr	Gln	Gln	Asn	Thr 735	Pro		
Ile	Gly	Asp	Gly 740	Pro	Val	Leu	Leu	Pro 745	Asp	Asn	His	Tyr	Leu 750	Ser	Tyr		
Gln	Ser	Ala 755	Leu	Ser	Lys	Asp	Pro 760		Glu	Lys	Arg	Asp 765		Met	.Val		
Leu	Leu 770	Glu	Phe	Val	Thr	Ala 775	Ala	Gly	Ile	Thr	Leu 780	Gly	Met	Asp	Glu		
<21: <21: <21: <21:	1> 2>	17 477 DNA Mous	e														
<40	_	17 +++	acca	catc	מכ כ	aadc	atca	c ac	ccac	atac	ctc	ccad	cca	ccaa	ggtccg		60
								•							ccggag	J	120
															ggtgcc		180
															gagagt	2	240
tcg	tcgt	ccg	agca	cgcc	ga g	cggc	cccc	g gg	gccc	cgca	gac	ccga	ccg	cggc	cccga	3	300

31/66

gccaagggca	agacccgggc	gagtcaggtg	aagccggggg	acagtictgcc	dcddcdcddd	360
cccggggccg	cggggccggg	ggcttcgggg	tccgggcacg	gagaggagcg	cggcgggggc	420
gccaaagcgt	cgcgctggcg	cgggaggcaa	aaccgggaga	aacgcttcac	gttcgtg	477

<210> 18 ·

<211> 159

<212> PRT

<213> Mouse

<400> 18

Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg Val Pro Pro Ser 1 5 10 15

Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly Gly Ala Asp Arg 20 25 30

Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly Pro Thr Gly Ala
35 40 45

Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala Pro Gly Glu Pro 50 55 60

Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp Leu Glu Glu Ser 65 70 75 80

Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro Arg Arg Pro Asp 85 90 95

Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser Gln Val Lys Pro 100 105 110

Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala Gly Pro Gly Ala 115 120 125

Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly Ala Lys Ala Ser 130 135 140

Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe Thr Phe Val 145 150 155

<210> 19

<211> 63

<212> DNA

<213> Mouse

<400> 19 cacgacttcc gacgcgcctt caagaagatc ctctgccgtg gggacagaaa acgcatcgtg	60
tga	63
<210> 20 <211> 20 <212> PRT <213> Mouse	
<400> 20	
His Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg 1 5 10 15	
Lys Arg Ile Val	
<210> 21 <211> 107 <212> DNA <213> homo sapiens	
<400> 21 ggatetteet ggeggegega egaeagetga ageagatgga gageeageet etgeeggggg	60
	.07
<210> 22 <211> 36 <212> PRT <213> homo sapiens	
<400> 22	
Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys Gln Met Glu Ser Gln 1 5 10 15	
Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr Leu Gln Lys Glu Val His 20 25 30	
Ala Ala Lys Ser 35	
<210> 23 <211> 369 <212> DNA <213> homo sapiens	
<400> 23 cgtatccgcg agttccgcca gaccttccgc aagatcattc gcagccacgt cctgaggcag	60

33/66

caagaacct	t tcaaggcagc	tggcaccagt	gcccgggtct	tggcagctca	tggcagtgac	120
ggagagcag	g tcagcctccg	tctcaacggc	cacccgccag	gagtgtgggc	caacggcagt	180
gctccccac	c ctgagcggag	gcccaatggc	tatgccctgg	ggctggtgag	tggagggagt	240
gcccaagag	t _. cccaggggaa	cacgggcctc	ccagacgtgg	agctccttag	ccatgagctc	300
aagggagtg	t gcccagagcc	ccctggccta	gatgaccccc	tggcccagga	tggagcagga	360
gtgtcctga						369
<210> 24						
<210> 24						

<210> 24

<211> 102

<212> PRT

<213> homo sapiens

<400> 24

Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser His 1 5 10 15

Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala Arg 20 25 30

Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg Leu 35 40 45

Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His Pro 50 55 60

Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly Ser 65 70 75 . 80

Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu Leu 85 90 95

Ser His Glu Leu Lys Gly 100

<210> 25

<211> 57

<212> DNA

<213> homo sapiens

<400> 25

accaagetge gggagaceaa egeeggeegg tgtgacacae ggeageagta eeggaag

57

<210> 26

<211> 19

<212 <213		PRT homo	sapi	ens												•
<400	> :	26														
Thr :	Lys	Leu	Arg	Glu 5	Thr	Asn	Ala	Gly	Arg 10	Cys	Asp	Thr	Arg	Gln 15	Gln	
Tyr .	Arg	Lys					·									
<210: <211: <212: <213:	> : > 1	27 393 DNA homo	sapi	ens											٠	
<400 gagg		27 aag d	etgag	gatca	ıa ga	aato	ettgg	, ago	cgct	:gga	cact	ggca	ict ç	ggact	:tcaag	60
cgaa	agg	cac c	gcago	ggga	ıg ca	gcag	ctat	ago	taco	gcc	ccat	ggtg	rtc d	ccaca	caagt	120
gtga	cca	atg t	cggc	cccc	g to	ıtggç	gacto	ggc	ctgo	ccc	tcaç	ccc	ecg o	cctac	tgccc	180
actg	cca	cca d	caac	ggco	a co	ctca	gcto	, cct	ggcc	atg	ccaa	gcca	ıgg ç	gacco	cagcc	240
ctgg	aga	ccc t	cgac	jacca	c ac	caco	etge	atg	gcto	gctc	ccaa	ggac	ga t	gggt	tcctc	300
aacg	gct	cct ç	gctca	ggco	et go	gacga	aggag	g gcc	etcto	ggc	ctga	gcgg	icc s	accto	gccctg	360
ctac	agg	aag a	gtgg	ggaga	c aç	tcat	gtga	ı tga	ì							393
<210 <211 <212 <213	> : > :	28 129. PRT homo	sapi	iens												
<400	> :	28														
Glu 1	Val	Gln	Ala	Glu 5	Ile	Lys	Lys	Ser	Trp 10	Ser	Arg	Trp	Thr	Leu 15	Ala	
Leu .	Asp	Phe	Lys 20	Arg	Ŀys	Ala	Arg	Ser 25	Gly	Ser	Ser	Ser	Tyr 30	Ser	Tyr	
Gly	Pro	Met 35	Val	Ser	His	Thr	Ser 40	Val	Thr	Asn	Val	Gly 45	Pro	Arg	Val	
	Leu 50	Gly	Leu	Pro	Leu	Ser 55	Pro	Arg	Leu	Leu	Pro 60	Thr	Ala	Thr	Thr	
Asn 65	Gly	His	Pro	Gln	Leu 70	Pro	Gly	His	Ala	Lys	Pro	Gly	Thr	Pro	Ala 80	

35/66

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp 90 Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser 105 100 Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val 120 125 Met <210> 29 <211> 264 <212> PRT <213> artificial sequence <220> <223> PTHR-cam7 amino acid sequence <400> 29 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 5 Leu Asp Phe Lys Arg Lys Ala Arg Ser Met Val Ser Lys Gly Glu Glu 20 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr 50 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 85 Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser 105 100

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp

120

115

36/66

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 130 135 140

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 145 150 155 160

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 165 170 175

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 180 185 190

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 195 200 205

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 210 215 220

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 225 230 235 240

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 245 250 . 255

Leu Gly Met Asp Glu Leu Tyr Lys 260

<210> 30

<211> 270

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam9 amino acid sequence

<400> 30

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Met 20 25 30

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 35 40 45

37/66

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
50 55 60

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 65 70 75 80

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 85 90 95

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln 100 105 110

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 115 120 125

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 130 135 140

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 145 150 155 160

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn . 165 170 175

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
· 180 185 190

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 195 200 205

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 210 215 220

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser 225 230 235 240

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val 245 250 255

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 260 · 265 270

<210> 31

<211> 272

<212> PRT ·

38/66

<213> artificial sequence

<220>

<223> PTHR-cam8 amino acid sequence

<400> 31

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 20 25 30

Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 35 40 45

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser 50 55 60

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe 65 70 75 80

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 85 90 95

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met 100 105 110

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 115 120 125

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 130 135 140

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 145 150 155 160

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu 165 170 175

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 180 185 190

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 195. 200 205

39/66

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 210 215 220

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala 225 230 235 240

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Glu 245 250 255

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 260 265 270

<210> 32

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam2 amino acid sequence

<400> 32

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 20 25 30

Gly Pro Met Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 35 . 40 . 45 .

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 50 55 60

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 65 70 75 80

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 85 90 95

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro 100 105 110

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 115 120 125

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

40/66

140 135 130 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 150 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 170 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 185 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr 235 230 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 245 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu 270 265 260 Leu Tyr Lys 275 <210> 33 <211> 289 <212> PRT <213> artificial sequence <220> <223> PTHR-cam5 amino acid sequence <400> 33 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 1 Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 25 20 Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val

40

45

41/66

Gly Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val 70 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys 90 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His 115 Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 130 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 155 145 150 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 170 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 180 185 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 195 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 210 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 225 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser 245 250 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 260 265 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr

42/66

275 280 285

Lys

<210> 34 <211> 325 <212> PRT <213> artificial sequence <220> <223> PTHR-cam1 amino acid sequence <400> 34

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala 65 70 75 80

Leu Glu Thr Leu Glu Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr 85 90 95

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
100 105 110

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys 115 120 125

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp 130 135 140

Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg 145 150 155 160

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro 165 170 · 175

43/66

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu 215 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met 230 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His 250 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn 270 260 265 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu 280 275 Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His 290 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met 320 Asp Glu Leu Tyr Lys 325 <210> 35 <211> 339 <212> PRT <213> artificial sequence <223> PTHR-cam4 amino acid sequence Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 5

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr

20

44/66

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 150 155 Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 180 185 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 200 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 235 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 245 250 255 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 260 265 270

45/66

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 280

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr 295 300

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 305 310

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu

Leu Tyr Lys

<210> 36 <211> 354

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam3 amino acid sequence

<400> 36

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 5 10

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 20 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val 35

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr 50

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala 65 70 75

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp 85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser 105

Gly	Pro	Glu 115	Met	Val	Ser	Lys	Gly 120	Glu	Glu	Leu	Phe	Thr 125	Gly	Val	Val
Pro	Ile 130	Leu	Val	Glu	Leu	Asp 135	Gly	Asp	Val	Asn	Gly 140	His	Lys	Phe	Ser
Val 145	Ser	Gly	Glu	Gly	Glu 150	Gly	Asp	Ala	Thr	Tyr 155	Gly	Lys ·	Leu	.Thr	Leu 160
Lys	Phe	Ile	Суз	Thr 165	Thr	Gly	Lys	Leu	Pro 170	Val	Pro	Trp	Pro	Thr 175	Leu
Val	Thr	Thr	Phe 180	Gly	Tyr	Gly	Leu	Gln 185	Cys	Phe	Ala	Arg	Tyr 190	Pro	Asp
His	Met	Lys 195	Gln	His	Asp	Phe	Phe 200	Lys	Ser	Ala	Met	Pro 205	Glu	Gly	Tyr
Val	Gln 210	Glu	Arg	Thr	Ile	Phe 215	Phe	Lys	Asp	Asp	Gly 220	Asn	Tyr	Lys	Thr
Arg 225	Ala	Glu	Val	Lys	Phe 230	Glu	Gly	Asp	Thr	Leu 235	Val	Asn	Arg	Ile	Glu 240
Leu	Lys	Gly	Ile	Asp 245	Phe	Lys	Glu	Asp	Gly 250	Asn	Ile	Leu	Gly	His 255	Lys
Leu	Glu	Tyr	Asn 260	Tyr	Asn	Ser	His	Asn 265	Val	Tyr	Ile	Met	Ala 270	Asp	Lys
Gln	Lys	Asn 275	_	Ile	Lys	Val	Asn 280	Phe	Lys	Ile	Arg	His 285		Ile	Glu
Asp	Gly 290		Val	Gln	Leu	Ala 295		His	Tyr	Gln	Gln 300		Thr	Pro	Ile
Gly 305		Gly	Pro	Val	Leu 310	Leu	Pro	Asp	Asn	His 315		Leu	Ser	Tyr	Gln 320
Ser	Ala	Leu	Ser	Lys 325	Asp	Pro	Asn	Glu	Lys 330		Asp	His	Met	Val 335	
Leu	Glu	. Phe	Val 340		Ala	Ala	Gly	Ile 345		Leu	Gly	Met	: Asp 350		Leu

47/66

Tyr Lys

<210> 37 <211> 368 <212> PRT <213> artificial sequence <220> <223> PTHR-cam10 amino acid sequence <400> 37 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 25 20 Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr 50 Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala 65 Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp 95 Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser 100 Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val 120 115 Met Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 135 . Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser 155 150 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe.

170

48/66

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 180 185 190

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met 195 200 205

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 210 215 220

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 225 230 235 240

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 245 250 255

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu 260 265 270

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 275 280 285

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 290 295 300

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 305 310 315 320

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala 325 330 335

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu 340 345 350

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 355 360 365

<210> 38

<211> 518

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-PTHR-FRETcontrol amino acid sequence

<400> 38

49/66

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Met Val Ser Lys Gly Glu Glu Leu 20 25 30

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn 35 40 45

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr 50 55 60

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 65 70 75 80

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 85 90 . 95

Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala 100 105 110

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 115 120 125

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 130 135 140

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 145 . 150 . 155 . 160

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 165 170 175

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 180 185 190

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 195 200 · 205

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Pro Asp Asn His 210 215 220

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 225 230 235 240

Asp	His	Met	Val	Leu 245	Leu	Glu	Phe	Val	Thr 250	Ala	Ala	Gly	Ile	Thr 255	Leu
Gly	Met	Asp	Glu 260	Leu	Tyr	Lys	Ser	Gly 265	Ser	Ser	Ser	Tyr	Ser 270	Tyr	Gly
Pro	Met	Val 275	Ser	His	Thr	Ser	Met 280	Val	Ser	Lys	Gly	Glu 285	Glu	Leu	Phe
Thr	Gly 290	Val	Val	Pro	Ile	Leu 295	Val	Glu	Leu	Asp	Gly 300	Asp	Val	Asn	Gly
His 305	Lys	Phe	Ser	Val	Ser 310	Gly	Glu	Gly	Glu	Gly 315	Asp	Ala	Thr	Tyr	Gly 320
Lys	Leu	Thr	Leu	Lys 325	Phe	Ile	Суз	Thr	Thr 330	Gly	Lys	Leu	Pro	Val 335	Pro
Trp	Pro	Thr	Leu 340	Val	Thr	Thr	Leu	Thr 345	Trp	Gly	Val	Gln	Cys 350	Phe	Ser
Arg	Tyr	Pro 355		His	Met	Lys	Gln 360	His	Asp	Phe	Phe	Lys 365	Ser	Ala	Met
Pro	Glu 370	_	Tyr	Val	Gln	Glu 375	Arg	Thr	Ile	Phe	Phe 380		Asp	Asp	Gly
Asn 385		: Lys	: Thr	Arg	Ala 390	Glu	Val	Lys	Phe	Glu 395		Asp	Thr	Leu	Val 400
Asn	Arg	J Ile	e Glu	1 Leu 405	Lys	Gly	Ile	Asp	Phe 410	e Lys	Glu	ı Asp	Gly	Asn 415	Ile
Leu	a Gly	y His	Lys 420		ı Glu	Tyr	Asn	Tyr 425		e Sei	His	s Asn	Val 430		Ile
Thi	c Ala	a Ası 43	_	s Glr	Lys	Asn	Gly 440		e Lys	s Ala	a Ası	n Phe 445	e Lys S	: Ile	Arg
His	3 As:	_	e Gl	u Ası	o Gly	/ Ser 455		Glr	n Let	u Ala	a Asj 46		з Туг	Glr	Gln
As:		r Pr	o Il	e Gl	y Asp 470		y Pro	o Va.	l Le	u Le 47		o As	Ası	n His	480

51/66

Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp 485 490 495

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly 500 505 510

Met Asp Glu Leu Tyr Lys 515

<210> 39

<211> 1737

<212> DNA

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 cDNA sequence

<400> 39 atgcccatca

atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc 60 120 atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc 180 ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 240 300 geotgetteg teetggteet caegeagage tecatettea gteteetgge categeeatt gaccgctaca ttgccatccg catcccgctc cggtacaatg gcttggtgac cgggacgagg 360 getaagggca tcattgccat etgetgggtg etgtegtttg ccateggcet gacteccatg 420 ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg 480 540 gagggccaag tggcctdtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc 600 aacttetttg cetgtgtget ggtgeecetg etgeteatge tgggtgteta tttgeggate tteetggegg egegaegaea getgaageag atggagagee agtgttgtee ggggtgttgt 660 gcacggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg 720 780 ctetttgece tetgetgget geecetacae ateateaact getteaettt ettetgeece: gactgcagec acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat 840 teggttgtga atecetteat etaegeetae egtateegeg agtteegeea gaeetteege 900 960 aagatcatte geagecaegt eetgaggeag caagaaeett teaaggeage tggeaeeagt 1020 gcccgggtct tggcagctca tggcagtgac ggagagcagg tcagcctccg tctcaacggt gtgagcaagg gcgaggagct gttcaccggg gtggtgccca tcctqgtcga gctggacggc 1080

52/66

gacgtaaacg	gccacaggtt	cagcgtgtcc	ggcgagggcg	agggcgatgc	cacctacggc	1140
aagctgaccc	tgaagttcat	ctgcaccacc	ggcaagctgc	ccgtgccctg	gcccaccctc	1200
gtgaccaccc	tgacctgggg	cgtgcagtgc	ttcagccgct	accccgacca	catgaagcag	1260
cacgacttct	tcaagtccgc	catgcccgaa	ggctacgtcc	aggagcgtac	catcttcttc	1320
aaggacgacg	gcaactacaa	gacccgcgcc	gaggtgaagt	tcgagggcga	caccctggtg	1380
aaccgcatcg	agctgaaggg	catcgacttc	aaggaggacg	gcaacatcct	ggggcacaag	1440
ctggagtaca	actacatcag	ccacaacgtc	tatatcaccg	ccgacaagca	gaagaacggc	1500
atcaaggccc	acttcaagat	ccgccacaac	atcgaggacg	gcagcgtgca	gctcgccgac	1560
cactaccage	agaacacccc	catcggcgac	ggccccgtgc	tgctgcccga	caaccactac	1620
ctgagcaccc	agtccgccct	gagcaaagac	cccaacgaga	agcgcgatca	catggtcctg	1680
ctggagttcg	tgaccgccgc	cgggatcact	ctcggcatgg	acgagctgta	caagtaa	1737

<210> 40

<211> 578

<212> PRT

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 amino acid sequence

<400> 40

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile 1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp 20 25 · 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile 70 75 80

· Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr 100 105 110

53/66

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn 135 140 Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly . 150 155 Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr 170 Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu 185 Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly 225 230 235 Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr 245 250 Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu 265 260 Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr 275 280 Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg 290 295 300 Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser 305 320 310 Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val

54/66

350 345 340 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser 360 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu ` 375 380 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr 420 Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr 440 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu 455 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 475 470 Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys 490 485 Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu 505 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 520 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu

55/66

Tyr Lys

<210>

41

1686 <211> DNA <213> artificial sequence <220> <223> A2A-FlashPG-CFP-C33 cDNA sequence <400> 41 atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc 60 atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc 120 180 accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc 240 ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 300 gcctgcttcg tcctggtcct cacgcagagc tccatcttca gtctcctggc catcgccatt gaccgctaca ttgccatccg catcccgctc cggtacaatg gcttggtgac cgggacgagg 360 gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg 420 ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg 480 gagggccaag tggcctgtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc 540 aacttetttg cetgtgtget ggtgeeeetg etgeteatge tgggtgteta tttgeggate 600 ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt 660 gcacggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg 720 ctctttgccc tctgctggct gcccctacac atcatcaact gcttcacttt cttctgcccc 780 gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat 840 900 teggttgtga atceetteat etaegeetae egtateegeg agtteegeea gaeetteege aagatcatte geageeaegt eetgaggeag caagaaeett teaaggeage tggeaeeagt 960 gcccgggtcg tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctggtcgag 1020 1080 ctggacggcg acgtaaacgg ccacaggttc agcgtgtccg gcgagggcga gggcgatgcc acctacggca agctgaccct gaagttcatc tgcaccaccg gcaagctgcc cgtgccctgg 1140 1200 cccaccctcg tgaccaccct gacctggggc gtgcagtgct tcagccgcta ccccgaccac atgaagcagc acgacttett caagteegee atgeeegaag getaegteea ggagegtaee 1260 atcttcttca aggacgacgg caactacaag accegegeeg aggtgaagtt cgagggegac 1320 accetggtga accgcatega getgaaggge ategaettea aggaggaegg caacateetg 1380

56/66

gggcacaagc tggagtacaa	ctacatcagc	cacaacgtct	atatcaccgc	cgacaagcag	1440
aagaacggca tcaaggccca	cttcaagatc	cgccacaaca	tcgaggacgg	cagcgtgcag	1500
ctcgccgacc actaccagca	gaacaccccc	atcggcgacg	gccccgtgct	gctgcccgac	1560
aaccactacc tgagcaccca	gtccgccctg	agcaaagacc	ccaacgagaa	gcgcgatcac	1620
atggtcctgc tggagttcgt	gaccgccgcc	gggatcactc	tcggcatgga	cgagctgtac	1680
aagtaa					1686

<210> 42

<211> 561

<212> PRT

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C33 amino acid sequence

<400> 42

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile 1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp 20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile 65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr 100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys 115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn 130 . 135 140

Asn 145	Cys	Gly	Gln	Pro	Lys 150	Glu	Gly	Lys	Asn	His 155	Ser	Gln	Gly	Cys	Gly 160
Glu	Gly	Gln	Val	Ala 165	Cys	Leu	Phe	Glu	Asp 170	Val	Val	Pro	Met	Asn 175	Tyr
Met	.Val	Tyr	Phe 180	Asn	Phe	Phe	Ala	Cys 185	Val	Leu	Val	Pro	Leu 190	Leu	Leu
Met	Leu	Gly 195	Val	Tyr	Leu	Arg	Ile 200	Phe	Leu	Ala	Ala	Arg 205	Arg	Gln	Leu
Lys	Gln 210	Met	Glu	Ser	Gln	Cys 215	Суз	Pro	Gly	Суз	Cys 220	Ala	Arg	Ser	Thr
Leu 225	Gln	Lys	Glu	Val	His 230	Ala	Ala	Lys	Ser	Leu 235	Ala	Ile	Ile	Val	Gly 240
Leu	Phe	Ala	Leu	Cys 245	Trp	Leu	Pro	Leu	His 250	Ile	Ile	Asn	Суз	Phe 255	Thr
Phe	Phe	Суз	Pro 260	Asp	Cys	Ser	His	Ala 265	Pro	Leu	Trp	Leu	Met 270	Tyr	Leu
Ala	Ile	Val 275	Leu	Ser	His	Thr	Asn 280	Ser	Val	Val	Asn	Pro 285	Phe	Ile	Tyr
Ala	Tyr 290	Arg	Ile	Arg	Glu	Phe 295	Arg	Gln	Thr	Phe	Arg 300	Lys	Ile	Ile	Arg
Ser 305	His	Val	Leu	Arg	Gln 310	Gln	Glu	Pro	Phe	Lys 315	Ala	Ala	Gly	Thr	Ser 320
Ala	Arg	Val	Val	Ser 325		Gly	Glu	Glu	Leu 330	Phe	Thr	Gly	Val ·	Val 335	Pro
Ile	Leu	Val	Glu 340	Leu	Asp	Gly	Asp	Val 345	Asn	Gly	His	Arg	Phe 350	Ser	Val
Ser	Gly	Glu 355	_	Glu	Gly	Asp	Ala 360	Thr	Tyr	Gly	Lys	Leu 365		Leu	Lys
Phe	Ile 370		Thr	Thr	Gly	Ъуs 375		Pro	Val	Pro	Trp 380		Thr	Leu	Val

58/66

Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His 385 390 395 400 Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 405 410 415 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 420 425 430 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 435 440 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 450 455 Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 465 470 Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp 485 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 505 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser 515 520 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 535 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys <210> 43 <211> 1788 <212> DNA <213> artificial sequence <220>

atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc

<223> A2A-CFP-ModelPG-C49 cDNA sequence

<400> 43

atcctgggca	atgtgctggt	gtgctgggcc	gtgtggctca	acagcaacct	gcagaacgtc	120
accaactact	ttgtggtgtc	actggcggcg	gccgacatcg	cagtgggtgt	gctcgccatc	180
ccctttgcca	tcaccatcag	caccgggttc	tgcgctgcct	gccacggctg	cctcttcatt	240
gcctgcttcg	tcctggtcct	çacgcagagc	tccatcttca	gtctcctggc	catcgccatt	300
gaccgctaca	ttgccatccg	catcccgctc	cggtacaatg	gcttggtgac	cggcacgagg	360
gctaagggca	tcattgccat	ctgctgggtg	ctgtcgtttg	ccatcggcct	gactcccatg	420
ctaggttgga	acaactgcgg	tcagccaaag	gagggcaaga	accactccca	gggctgcggg	480
gagggccaag	tggcctgtct	ctttgaggat	gtggtcccca	tgaactacat	ggtgtacttc	540
aacttctttg	cctgtgtgct	ggtgcccctg	ctgctcatgc	tgggtgtcta	tttgcggatc	·600
ttcctggcgg	cgcgacgaca	gctgaagcag	atggagagcc	agectetgée	gggggagcgg	660
gcacggtcca	cactgcagaa	ggaggtccat	gctgccaagt	cactggccat	cattgtgggg	720
ctctttgccc	tctgctggct	gcccctacac	atcatcaact	gcttcacttt	cttctgcccc	780
gactgcagcc	acgcccctct	ctggctcatg	tacctggcca	tcgtcctctc	ccacaccaat	840
tcggttgtga	atcccttcat	ctacgcctac	cgtatccgcg	agttccgcca	gaccttccgc	900
aagatcattc	gcagccacgt	cctgaggcag	caagaacctt	tcaaggcagc	tggcaccagt	960
gcccgggtct	tggcagctca	tggcagtgac	ggagagcagg	tcagcctccg	tctcaacggc	1020
gtgagcaagg	gcgaggagct	gttcaccggg	gtggtgccca	tcctggtcga	gctggacggc	1080
gacgtaaacg	gccacaggtt	cagcgtgtcc	ggcgagggcg	agggcgatgc	cacctacggc	1140
aagctgaccc	tgaagttcat	ctgcaccacc	ggcaagctgc	ccgtgccctg	gcccaccctc	1200
gtgaccaccc	tgacctgggg	cgtgcagtgc	ttcagccgct	accccgacca	catgaagcag	1260
cacgacttct	tcaagtccgc	catgcccgaa	ggctacgtcc	aggagcgtac	catcttcttc	1320
aaggacgacg	gcaactacaa	gacccgcgcc	gaggtgaagt	tcgagggcga	caccctggtg	1380
aaccgcatcg	agctgaaggg	catcgacttc	aaggaggacg	gcaacatcct	ggggcacaag	1440
ctggagtaca	actacatcag	ccacaacgtc	tatatcaccg	ccgacaagca	gaagaacggc	1500
atcaaggccc	acttcaagat	ccgccacaac	atcgaggacg	gcagcgtgca	gctcgccgac.	1560
cactaccage	agaacacccc	catcggcgac	ggccccgtgc	tgctgcccga	caaccactac	1620
ctgagcaccc	agtccgccct	gagcaaagac	cccaacgaga	agcgcgatca	catggtcctg	1680
ctggagttcg	tgaccgccgc	cgggatcact	ctcggcatgg	acgagctgta	caaggctgag	1740
gctgcagcgc	gcgaagcatg	ctacccaaat	tattacacte	gcgcatga		1788

60/66

<210> 44 <211> 595 <212> PRT <213> artificial sequence <220> <223> A2A-CFP-ModelPG-C49 amino acid sequence Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile 5 Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu 40 Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu 95 Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn 135 Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly 155 150 Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr 170 165 Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu

185

180

61/66

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr 215 Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly 225 230 235 Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr 250 Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu 265 Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser 315 Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu 325 Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val 345 340 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser 360 355 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu 375 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu 385 Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp 405 His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr

420 . 425

62/66

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr 440 435 445 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu 450 455 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 465 Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys 485 495 Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu 500 505 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 515 520 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln 530 535 540 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu 545 550 555 560 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu 565 570 575 Tyr Lys Ala Glu Ala Ala Ala Arg Glu Ala Cys Cys Pro Gly Cys Cys Ala Arg Ala 595 <210> 45 <211> 1737 <212> DNA <213> artificial sequence <220> <223> A2A-CFP-C49 cDNA sequence <400> 45 atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc 60 atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc 120 180 accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc

ccctttgcca	tcaccatcag	caccgggttc	tgcgctgcct	gccacggctg	cctcttcatt	240
gcctgcttcg	tectggtect	cacgcagagc	tccatcttca	gtctcctggc	catcgccatt	300
gaccgctaca	ttgccatccg	catcccgctc	cggtacaatg	gcttggtgac	cggcacgagg	360
gctaagggca	tcattgccat	ctgctgggtg	ctgtcgtttg	ccatcggcct	gactcccatg	420
ctaggttgga	acaactgcgg	tcagccaaag	gagggcaaga	accactccca	gggctgcggg	480
gagggccaag	tggcctgtct	ctttgaggat	gtggtcccca	tgaactacat	ggtgtacttc	540
aacttctttg	cctgtgtgct	ggtgcccctg	ctgctcatgc	tgggtgtcta	tttgcggatc	600
ttcctggcgg	cgcgacgaca	gctgaagcag	atggagagcc	agcctctgcc	gggggagcgg	660
gcacggtcca	cactgcagaa	ggaggtccat	gctgccaagt	cactggccat	cattgtgggg	720
ctctttgccc	tetgetgget	gcccctacac	atcatcaact	gcttcacttt	cttctgcccc	780
gactgcagcc	acgcccctct	ctggctcatg	tacctggcca	tcgtcctctc	ccacaccaat	840
tcggttgtga	atcccttcat	ctacgcctac	cgtatccgcg	agttccgcca	gaccttccgc	900
aagatcattc	gcagccacgt	cctgaggcag	caagaacctt	tcaaggcagc	tggcaccagt	960
gcccgggtct	tggcagctca	tggcagtgac	ggagagcagg	tcagcctccg	tctcaacggt	1020
gtgagcaagg	gcgaggagct	gttcaccggg	gtggtgccca	tcctggtcga	gctggacggc	1080
gacgtaaacg	gccacaggtt	cagcgtgtcc	ggcgagggcg	agggcgatgc	cacctacggc	1140
aagctgaccc	tgaagttcat	ctgcaccacc	ggcaagctgc	cegtgeeetg	gcccaccctc	1200
gtgaccaccc	tgacctgggg	cgtgcagtgc	ttcagccgct	accccgacca	catgaagcag	1260
cacgacttct	tcaagtccgc	catgcccgaa	ggctacgtcc	aggagcgtac	catcttcttc	1320
aaggacgacg	gcaactacaa	gacccgcgcc	gaggtgaagt	tcgagggcga	caccctggtg	1380
aaccgcatcg	agctgaaggg	catcgacttc	aaggaggacg	gcaacatcct	ggggcacaag	1440
ctggagtaca	actacatcag	ccacaacgtc	tatatcaccg	ccgacaagca	gaagaacggc	1500
atcaaggccc	acttcaagat	ccgccacaac	atcgaggacg	gcagcgtgca	gctcgccgac	1560
cactaccage	agaacacccc	catcggcgac	ggccccgtgc	tgctgcccga	caaccactac	1620
ctgagcaccc	agtccgccct	gagcaaagac	cccaacgaga	agcgcgatca	catggtcctg	1680
ctggagttcg	tgaccgccgc	cgggatcact	ctcggcatgg	acgagctgta	caagtaa	1737

<210> 46 <211> 578 <212> PRT <213> artificial sequence

64/66

<220> <223> A2A-CFP-C49 amino acid sequence <400> 46 Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp 30 . Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile 50 Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile 70. Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu 85 . Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr 100 105 Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys 115 120 Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn 130 135 Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr 170 Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu 185

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr 210 215 220

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu 195 200 205

Leu 225	Gln	Lys	Glu	Val	His 230	Ala	Ala	Lys	Ser	Leu 235	Ala	Ile	Ile	Val	Gly 240
Leu	Phe	Ala ·	Leu	Cys 245	Trp	Leu	Pro	Leu	His 250	Ile	Ile	Asn	Cys	Phe 255	Thr
Phe	Phe	Cys	Pro 260	Asp	Суз	Ser	His	Ala 265	Pro	Leu	Trp	Leu	Met 270	Tyr	Leu
Ala	Ile	Val 275	Leu	Ser	His	Thr	Asn 280	Ser	Val	Val	Asn	Pro 285	Phe	Ile	Tyr
Ala	Туг 290	Arg	Ile	Arg	Glu	Phe 295	Arg	Gln	Thr	Phe	Arg 300	Lys	Ile	Ile	Arg .
Ser 305	His	Val	Leu	Arg	Gln 310	Gln	Glu	Pro	Phe	Lys 315	Ala	Ala	Gly	Thr	Ser 320
Ala	Arg	Val	Leu	Ala 325	Ala	His	Gly	Ser	Asp 330	Gly	Glu	Gln	Val	Ser 335	Leu
Arg	Leu	Asn	Gly 340	Val	Ser	Lys	Gly	Glu 345	Glu	Leu	Phe	Thr	Gly 350	Val	Val
Pro	Ile	Leu 355	Val	Glu	Leu	Asp	Gly 360	Asp	Val	Asn	Gly	His 365	Arg	Phe	Ser
Val	Ser 370	Gly	Glu	Gly	Glu	Gly 375	Asp	Ala	Thr	Tyr	Gly 380	Lys	Leu	Thr	Leu
Lys 385	Phe	Ile	Суз	Thr	Thr 390		Lys	Leu	Pro	Val 395	Pro	Trp	Pro	Thr	Leu 400
Val	Thr	Thr	Leu	Thr 405		Gly	Val	Gln	Cys 410	Phe	Ser	Arg	Tyr	Pro 415	Asp
His	Met	Lys	Gln 420		Asp	Phe	Phe	Lys 425	Ser	Ala	Met	Pro	Glu 430	-	Tyr
Val	Gln	Glu 435		Thr	Ile	Phe	Phe 440		Asp	Asp	Gly	Asn 445		Lys	Thr
Arg	Ala	Glu ·	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu

66/66

450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485
490
495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln 530 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu 545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu 565 570 575

Tyr Lys

50/66